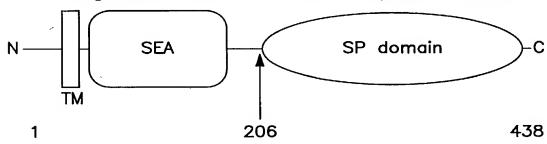
Domain organization and amino acid sequence of MTSP7

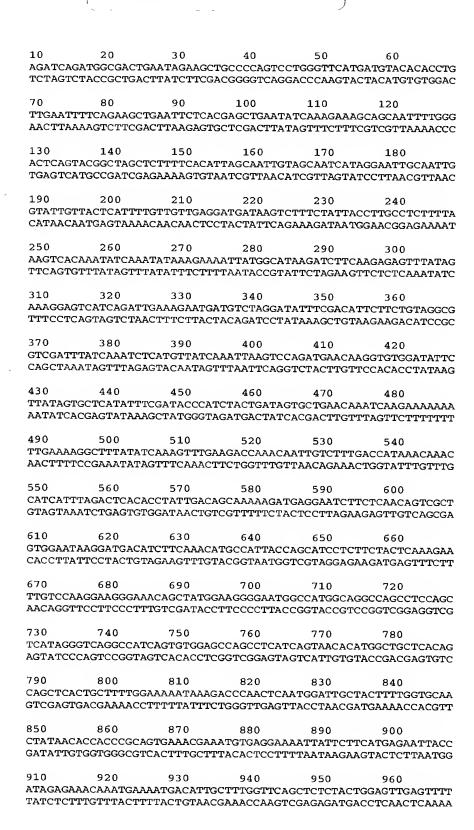


10 MMYTPVEFSEAE	20		40 CLAIVAIIGIA	50 LIGIVTHFVVE	60 DDKSFY
70 YLASFKVTNIKY		90 FIERSHQIERN		110 GGRFIKSHVI	120 KLSPDE
130 QGVDILIVLIFF		150 KKIEKALYQSI		170 KPSFRLTPID	180 SKKMRN
190 LLNSRCGIRMTS	200 SSNMPLPASSST(1 210 DRIVQGRETAN	220 MEGEWPWQASI	230 LQLIGSGHQCG	240 SASLISN
250 TWLLTAAHCFWK	260	270	280	290	300
310 TGVEFSNIVORV	320	330	340	350	360
370 KDVYDGLITPGN	380	390	400	410	420
430	HCAOLIMORIDA	ionobboot E	, 1511115111111	, GI VONGQDOL	

VYTRVTKYRDWIASKTGM*

▼ = protease cleavage site

FIG. I



HELLER EHRMAN WHITE & MCAULIFFE LIP

Sheet 3 of 4 g per group grou

TRANSMEMBRANE SERING PROTESSET, THE ENCODED POLYPEPTIDES AND METHODS BASED THEREON

Applicant: Edwin Madison et al Filed March 13, 2002 Appl No. 10/099,700 Examiner: Unassigned Art Unit

Art Unit. Unassigned Our Docket No.: 24745-1613

CAAATATAGTCCAGAGAGTTTGCCTCCCAGACTCATCTATAAAGTTGCCACCTAAAACAA GTTTATATCAGGTCTCTCAAACGGAGGGTCTGAGTAGATATTTCAACGGTGGATTTTGTT

GTGTGTTCGTCACAGGATTTGGATCCATTGTAGATGATGGACCTATACAAAATACACTTC CACACAAGCAGTGTCCTAAACCTAGGTAACATCTACTACCTGGATATGTTTTATGTGAAG

GGCAAGCCAGAGTGGAAACCATAAGCACTGATGTGTAACAGAAAGGATGTGTATGATG ${\tt CCGTTCGGTCTCACCTTTGGTATTCGTGACTACACACATTGTCTTTCCTACACATACTAC}$

AGGGAGATTCTGGTGGACCTCTGGTTTATGATAATCATGACATCTGGTACATTGTAGGTA TCCCTCTAAGACCACCTGGAGACCAAATACTATTAGTACTGTAGACCATGTAACATCCAT

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 $\tt CCTGAGGTGGCCTTTACATACGTAGGACCAAACCCTCTCTACCATGAGGGAAGAAGACAC$ GGACTCCACCGGAAATGTATGCATCCTGGTTTGGGAGAGATGGTACTCCCTTCTTCTGTG

AGCAAATGACAGACACCTATTCCTTACTCACAAGGGAAACTGCTTGTGATACTTCCT TCGTTTACTGTCTGTCGTGGATAAGGAATGAGTGTTCCCTTTGACGAACACTATGAAGGA

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GGGCTTATATCTAATAATACAGAGCACTATCACTAACCTCAACAGTTGACATTTTAAAAG CCCGAATATAGATTATTATGTCTCGTGATAGTGATTGGAGTTGTCAACTGTAAAATTTTC

 ${\tt TTTTAAATGTATCTGAACTTGCTGTTAACACAGTGTTATAACTCAAGCACTAGCTTCAG}$

GAAGCATGTTGTTTAAGAGCTTTTTCTGATTTATTCTTTAACAGCATCTTGCCATC $\tt CTTCGTACAACAACAATTCTTCGAAAAGACTAAATAAGAAATTGTCGTAGAACGGTAG$

AAAAATTTACATAGACTTGAACGACAATTGTGTCACAATATTGAGTTCGTGATCGAAGTC